

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: KOSHIBA, TOMOKAZU

(ii) TITLE OF INVENTION: ALDEHYDE OXIDASE GENE DERIVED FROM PLANT  
AND UTILIZATION THEREOF

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP  
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(C) CITY: FALLS CHURCH  
(D) STATE: VIRGINIA  
(E) COUNTRY: UNITED STATES OF AMERICA  
(F) ZIP: 22040-0747

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/943,144  
(B) FILING DATE: 03-OCT-1997  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: STEWART, RAYMOND C.  
(B) REGISTRATION NUMBER: 21,066  
(C) REFERENCE/DOCKET NUMBER: 2185-208P

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703)205-8000  
(B) TELEFAX: (703)205-8050

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4412 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: maize (Zea mays L.)  
(B) STRAIN: cultivar: Golden Cross Bantam 70

## (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 46..4119

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGCTGTGTT GTGCTGTGCT GCGTGCTGTG GAGGGGGAGG AGGAG ATG GGG AAG	54
Met Gly Lys	
1	
GAG GCA GGG GCA GCG GAG TCG TCG ACG GTG GTG CTG GCC GTC AAC GGC	102
Glu Ala Gly Ala Ala Glu Ser Ser Thr Val Val Leu Ala Val Asn Gly	
5 10 15	
AAG CGC TAC GAG GCG GCC GGC GTG GCT CCG TCC ACG TCG CTG CTG GAG	150
Lys Arg Tyr Glu Ala Ala Gly Val Ala Pro Ser Thr Ser Leu Leu Glu	
20 25 30 35	
TTC CTC CGC ACC CAG ACG CCC GTC AGA GGC CCC AAG CTC GGC TGC GGC	198
Phe Leu Arg Thr Gln Thr Pro Val Arg Gly Pro Lys Leu Gly Cys Gly	
40 45 50	
GAA GGT GGC TGC GGT GCA TGC GTG GTC CTC GTC TCC AAG TAC GAC CCG	246
Glu Gly Gly Ala Cys Val Val Leu Val Ser Lys Tyr Asp Pro	
55 60 65	
GCC ACG GAC GAG GTG ACC GAG TTC TCT GCC AGC TCC TGC CTG ACG CTG	294
Ala Thr Asp Glu Val Thr Glu Phe Ser Ala Ser Ser Cys Leu Thr Leu	
70 75 80	
CTC CAC AGC GTG GAC CGC TGC TCA GTG ACC ACC AGC GAG GGA ATC GGC	342
Leu His Ser Val Asp Arg Cys Ser Val Thr Thr Ser Glu Gly Ile Gly	
85 90 95	
AAC ACC AGG GAT GGC TAC CAC CCC GTG CAG CAG CGC CTC TCC GGC TTC	390
Asn Thr Arg Asp Gly Tyr His Pro Val Gln Gln Arg Leu Ser Gly Phe	
100 105 110 115	
CAC GCC TCG CAG TGC GGC TTC TGC ACA CCC GGC ATG TGC ATG TCC ATC	438
His Ala Ser Gln Cys Gly Phe Cys Thr Pro Gly Met Cys Met Ser Ile	
120 125 130	
TTC TCC GCC CTT GTC AAG GCC GAC AAC AAG TCC GAT CGC CCG GAC CCT	486
Phe Ser Ala Leu Val Lys Ala Asp Asn Lys Ser Asp Arg Pro Asp Pro	
135 140 145	
CCT GCT GGC TTC TCC AAG ATC ACT ACC TCG GAG GCA GAG AAG GCT GTC	534
Pro Ala Gly Phe Ser Lys Ile Thr Thr Ser Glu Ala Glu Lys Ala Val	
150 155 160	
TCG GGC AAC CTT TGT CGT TGC ACC GGA TAC AGA CCC ATT GTT GAC ACC	582
Ser Gly Asn Leu Cys Arg Cys Thr Gly Tyr Arg Pro Ile Val Asp Thr	
165 170 175	
TGC AAA AGC TTT GCC TCT GAT GTT GAC CTC GAG GAC CTA GGC CTC AAC	630

- Cys Lys Ser Phe Ala Ser Asp Val Asp Leu Glu Asp Leu Gly Leu Asn	180	185	190	195	
TGT TTC TGG AAG AAG GGC GAA GAA CCT GCA GAA GTC AGC AGG CTG CCG					678
Cys Phe Trp Lys Lys Gly Glu Pro Ala Glu Val Ser Arg Leu Pro	200		205	210	
GGG TAC AAC AGC GGT GCC GTC TGC ACC TTT CCA GAG TTT CTC AAA TCC					726
Gly Tyr Asn Ser Gly Ala Val Cys Thr Phe Pro Glu Phe Leu Lys Ser	215	220		225	
GAA ATC AAG TCT ACT ATG AAG CAG GTG AAC GAT GTC CCC ATT GCA GCC					774
Glu Ile Lys Ser Thr Met Lys Gln Val Asn Asp Val Pro Ile Ala Ala	230	235		240	
TCA GGT GAT GGC TGG TAC CAT CCT AAG AGC ATT GAA GAG CTT CAC AGG					822
Ser Gly Asp Gly Trp Tyr His Pro Lys Ser Ile Glu Glu Leu His Arg	245	250	255		
TTG TTT GAT TCC AGC TGG TTT GAT GAC AGT TCT GTG AAG ATT GTT GCT					870
Leu Phe Asp Ser Ser Trp Phe Asp Asp Ser Ser Val Lys Ile Val Ala	260	265	270	275	
TCA AAC ACT GGG TCT GGA GTG TAC AAG GAT CAG GAC CTC TAC GAC AAG					918
Ser Asn Thr Gly Ser Gly Val Tyr Lys Asp Gln Asp Leu Tyr Asp Lys	280		285	290	
TAC ATT GAC ATC AAA GGA ATC CCA GAG CTT TCA GTC ATC AAT AAA AAC					966
Tyr Ile Asp Ile Lys Gly Ile Pro Glu Leu Ser Val Ile Asn Lys Asn	295		300	305	
GAC AAA GCA ATT GAG CTT GGA TCA GTT GTG TCC ATC TCT AAA GCT ATT					1014
Asp Lys Ala Ile Glu Leu Gly Ser Val Val Ser Ile Ser Lys Ala Ile	310	315		320	
GAA GTG CTG TCA GAT GGA AAT TTG GTC TTC AGA AAG ATT GCT GAT CAC					1062
Glu Val Leu Ser Asp Gly Asn Leu Val Phe Arg Lys Ile Ala Asp His	325	330	335		
CTC AAC AAA GTG GCT TCA CCG TTT GTT CGG AAC ACT GCA ACC ATA GGA					1110
Leu Asn Lys Val Ala Ser Pro Phe Val Arg Asn Thr Ala Thr Ile Gly	340	345	350	355	
GGA AAC ATA ATG ATG GCA CAA AGG TTG CCA TTT GAA TCG GAT GTT GCA					1158
Gly Asn Ile Met Met Ala Gln Arg Leu Pro Phe Glu Ser Asp Val Ala	360		365	370	
ACC GTG CTC CTA GCT GCG GGT TCG ACA GTC ACA GTC CAG GTG GCT TCC					1206
Thr Val Leu Leu Ala Ala Gly Ser Thr Val Thr Val Gln Val Ala Ser	375	380		385	
AAA AGG CTG TGC TTC ACT CTG GAG GAA TTC TTG GAA CAA CCT CCA TGT					1254
Lys Arg Leu Cys Phe Thr Leu Glu Glu Phe Leu Glu Gln Pro Pro Cys	390	395		400	
GAT TCT AGG ACC CTG CTG CTG AGC ATA TTT ATC CCA GAA TGG GGT TCA					1302

-Asp	Ser	Arg	Thr	Leu	Leu	Ser	Ile	Phe	Ile	Pro	Glu	Trp	Gly	Ser		
405				410						415						
GAC	TAT	GTC	ACC	TTT	GAG	ACT	TTC	CGA	GCC	GCC	CCA	CGA	CCA	TTT	GGA	1350
Asp	Tyr	Val	Thr	Phe	Glu	Thr	Phe	Arg	Ala	Ala	Pro	Arg	Pro	Phe	Gly	
420				425					430					435		
AAT	GCT	GTC	TCT	TAT	GTA	AAC	TCT	GCT	TTC	TTG	GCA	AGG	ACA	TCA	GGC	1398
Asn	Ala	Val	Ser	Tyr	Val	Asn	Ser	Ala	Phe	Leu	Ala	Arg	Thr	Ser	Gly	
									445					450		
AGC	CTT	CTA	ATT	GAG	GAT	ATA	TGC	TTG	GCA	TTT	GGT	GCC	TAC	GGA	GTC	1446
Ser	Leu	Leu	Ile	Glu	Asp	Ile	Cys	Leu	Ala	Phe	Gly	Ala	Tyr	Gly	Val	
								455		460			465			
GAT	CAT	GCC	ATC	AGA	GCT	AAG	AAG	GTT	GAA	GAT	TTC	TTG	AAG	GGA	AAA	1494
Asp	His	Ala	Ile	Arg	Ala	Lys	Lys	Val	Glu	Asp	Phe	Leu	Lys	Gly	Lys	
						470		475				480				
TCG	CTG	AGC	TCA	TTT	GTG	ATA	CTT	GAA	GCA	ATT	AAA	CTA	CTC	AAA	GAT	1542
Ser	Leu	Ser	Ser	Phe	Val	Ile	Leu	Glu	Ala	Ile	Lys	Leu	Leu	Lys	Asp	
						485		490			495					
ACC	GTT	TCA	CCA	TCA	GAA	GGC	ACT	ACA	CAT	CAT	GAA	TAC	AGG	GTC	AGC	1590
Thr	Val	Ser	Pro	Ser	Glu	Gly	Thr	Thr	His	His	Glu	Tyr	Arg	Val	Ser	
						500		505			510			515		
TTG	GCT	GTC	AGT	TTC	TTG	TTC	AGT	TTC	TTA	TCT	TCC	CTT	GCC	AAC	AGT	1638
Leu	Ala	Val	Ser	Phe	Leu	Phe	Ser	Phe	Leu	Ser	Ser	Leu	Ala	Asn	Ser	
						520		525			530					
TCG	AGT	GCA	CCA	TCA	AAT	ATT	GAT	ACT	CCC	AAT	GGG	TCA	TAT	ACT	CAT	1686
Ser	Ser	Ala	Pro	Ser	Asn	Ile	Asp	Thr	Pro	Asn	Gly	Ser	Tyr	Thr	His	
						535		540			545					
GAA	ACT	GGT	AGC	AAT	GTG	GAC	TCA	CCT	GAG	AGG	CAT	ATT	AAG	GTT	GAC	1734
Glu	Thr	Gly	Ser	Asn	Val	Asp	Ser	Pro	Glu	Arg	His	Ile	Lys	Val	Asp	
						550		555			560					
AGC	AAT	GAT	TTG	CCA	ATT	CGT	TCA	AGA	CAA	GAA	ATG	GTT	TTC	AGC	GAT	1782
Ser	Asn	Asp	Leu	Pro	Ile	Arg	Ser	Arg	Gln	Glu	Met	Val	Phe	Ser	Asp	
						565		570			575					
GAG	TAC	AAG	CCT	GTT	GGC	AAG	CCG	ATC	AAG	AAA	GTC	GGG	GCA	GAG	ATC	1830
Glu	Tyr	Lys	Pro	Val	Gly	Lys	Pro	Ile	Lys	Lys	Val	Gly	Ala	Glu	Ile	
						580		585			590			595		
CAA	GCA	TCA	GGG	GAG	GCT	GTG	TAC	GTT	GAT	GAT	ATC	CCT	GCT	CCC	AAG	1878
Gln	Ala	Ser	Gly	Glu	Ala	Val	Tyr	Val	Asp	Asp	Ile	Pro	Ala	Pro	Lys	
						600		605			610			610		
GAT	TGC	CTC	TAT	GGA	GCA	TTT	ATC	TAC	AGC	ACA	CAT	CCT	CAT	GCT	CAT	1926
Asp	Cys	Leu	Tyr	Gly	Ala	Phe	Ile	Tyr	Ser	Thr	His	Pro	His	Ala	His	
						615		620			625					
GTG	AGA	AGT	ATC	AAC	TTC	AAA	TCA	TCC	TTG	GCT	TCA	CAG	AAG	GTC	ATC	1974

-Val Arg Ser Ile Asn Phe Lys Ser Ser Leu Ala Ser Gln Lys Val Ile		630	635	640	
ACA GTT ATA ACC GCA AAG GAT ATT CCA AGC GGT GGA GAA AAT ATT GGA	2022				
Thr Val Ile Thr Ala Lys Asp Ile Pro Ser Gly Gly Glu Asn Ile Gly		645	650	655	
AGC AGC TTC CTG ATG CAA GGA GAA GCA CTA TTT GCA GAT CCA ATC GCT	2070				
Ser Ser Phe Leu Met Gln Gly Glu Ala Leu Phe Ala Asp Pro Ile Ala		660	665	670	675
GAA TTT GCT GGT CAA AAT ATT GGT GTC GTG ATT GCT GAA ACA CAA AGA	2118				
Glu Phe Ala Gly Gln Asn Ile Gly Val Val Ile Ala Glu Thr Gln Arg		680	685	690	
TAT GCT AAT ATG GCT GCA AAG CAA GCT GTT GAG TAT AGC ACA GAA	2166				
Tyr Ala Asn Met Ala Ala Lys Gln Ala Val Val Glu Tyr Ser Thr Glu		695	700	705	
AAT CTG CAG CCA CCA ATT CTG ACA ATA GAA GAT GCC ATC CAA AGA AAC	2214				
Asn Leu Gln Pro Pro Ile Leu Thr Ile Glu Asp Ala Ile Gln Arg Asn		710	715	720	
AGC TAC ATC CAA ATT CCC CCA TTT TTA GCT CCA AAG CCA GTT GGT GAC	2262				
Ser Tyr Ile Gln Ile Pro Pro Phe Leu Ala Pro Lys Pro Val Gly Asp		725	730	735	
TAC AAC AAA GGG ATG GCT GAA GCA GAC CAC AAG ATT CTA TCA GCA GAG	2310				
Tyr Asn Lys Gly Met Ala Glu Ala Asp His Lys Ile Leu Ser Ala Glu		740	745	750	755
GTA AAA CTT GAA TCC CAG TAC TTC TAC ATG GAA ACT CAA GCA GCA	2358				
Val Lys Leu Glu Ser Gln Tyr Tyr Phe Tyr Met Glu Thr Gln Ala Ala		760	765	770	
CTA GCG ATT CCT GAT GAA GAT AAC TGC ATA ACA ATC TAT TCC TCG ACA	2406				
Leu Ala Ile Pro Asp Glu Asp Asn Cys Ile Thr Ile Tyr Ser Ser Thr		775	780	785	
CAA ATG CCT GAG CTC ACA CAA AAT TTG ATA GCA AGG TGT CTT GGC ATT	2454				
Gln Met Pro Glu Leu Thr Gln Asn Leu Ile Ala Arg Cys Leu Gly Ile		790	795	800	
CCA TTT CAC AAT GTC CGT GTC ATC AGC AGA AGA GTA GGA GGA GGC TTT	2502				
Pro Phe His Asn Val Arg Val Ile Ser Arg Arg Val Gly Gly Gly Phe		805	810	815	
GGT GGA AAG GCA ATG AAA GCA ACG CAT ACT GCA TGT GCA TGT GCC CTT	2550				
Gly Gly Lys Ala Met Lys Ala Thr His Thr Ala Cys Ala Cys Ala Leu		820	825	830	835
GCT GCC TTC AAG CTG CGG CGT CCA GTT AGG ATG TAC CTC GAT CGC AAG	2598				
Ala Ala Phe Lys Leu Arg Arg Pro Val Arg Met Tyr Leu Asp Arg Lys		840	845	850	
ACG GAC ATG ATA ATG GCT GGA GGG AGA CAT CCA ATG AAG GCG AAG TAC	2646				

-Thr Asp Met Ile Met Ala Gly Gly Arg His Pro Met Lys Ala Lys Tyr		
855	860	865
TCT GTT GGG TTC AAG TCA GAT GGC AAG ATC ACA GCC TTG CAC CTA GAT		2694
Ser Val Gly Phe Lys Ser Asp Gly Lys Ile Thr Ala Leu His Leu Asp		
870	875	880
CTT GGA ATC AAT GCT GGA ATA TCA CCA GAT GTG AGT CCA TTG ATG CCA		2742
Leu Gly Ile Asn Ala Gly Ile Ser Pro Asp Val Ser Pro Leu Met Pro		
885	890	895
CGT GCT ATC ATA GGA GCT CTC AAA AAG TAC AAC TGG GGC ACT CTT GAA		2790
Arg Ala Ile Ile Gly Ala Leu Lys Lys Tyr Asn Trp Gly Thr Leu Glu		
900	905	910
915		
TTT GAC ACC AAG GTC TGC AAG ACA AAT GTC TCA TCA AAG TCA GCA ATG		2838
Phe Asp Thr Lys Val Cys Lys Thr Asn Val Ser Ser Lys Ser Ala Met		
920	925	930
CGA GCT CCT GGA GAT GTG CAG GGC TCT TTC ATC GCT GAA GCC ATC ATC		2886
Arg Ala Pro Gly Asp Val Gln Gly Ser Phe Ile Ala Glu Ala Ile Ile		
935	940	945
GAG CAT GTT GCC TCA GCA CTC GCA CTA GAC ACT AAC ACC GTC AGG AGG		2934
Glu His Val Ala Ser Ala Leu Ala Leu Asp Thr Asn Thr Val Arg Arg		
950	955	960
AAG AAC CTT CAT GAT TTT GAA AGC CTT GAA GTT TTC TAT GGA GAA AGT		2982
Lys Asn Leu His Asp Phe Glu Ser Leu Glu Val Phe Tyr Gly Glu Ser		
965	970	975
GCA GGT GAA GCT TCT ACA TAC AGC CTG GTT TCC ATG TTT GAC AAG CTG		3030
Ala Gly Glu Ala Ser Thr Tyr Ser Leu Val Ser Met Phe Asp Lys Leu		
980	985	990
995		
GCC TTG TCT CCA GAA TAC CAG CAC AGG GCT GCA ATG ATT GAG CAG TTC		3078
Ala Leu Ser Pro Glu Tyr Gln His Arg Ala Ala Met Ile Glu Gln Phe		
1000	1005	1010
AAT AGC AGC AAC AAA TGG AAG AAA CGC GGC ATT TCT TGT GTG CCA GCC		3126
Asn Ser Ser Asn Lys Trp Lys Lys Arg Gly Ile Ser Cys Val Pro Ala		
1015	1020	1025
ACT TAT GAG GTT AAT CTT CGA CCA ACT CCA GGC AAG GTG TCA ATC ATG		3174
Thr Tyr Glu Val Asn Leu Arg Pro Thr Pro Gly Lys Val Ser Ile Met		
1030	1035	1040
AAT GAT GGT TCC ATC GCT GTC GAG GTT GGA GGA ATT GAG ATA GGT CAA		3222
Asn Asp Gly Ser Ile Ala Val Glu Val Gly Gly Ile Glu Ile Gly Gln		
1045	1050	1055
GGA TTG TGG ACT AAA GTG AAG CAG ATG ACG GCC TTT GGA CTG GGA CAG		3270
Gly Leu Trp Thr Lys Val Lys Gln Met Thr Ala Phe Gly Leu Gly Gln		
1060	1065	1070
1075		
CTG TGT CCT GAT GGT GGC GAA TGC CTT CTG GAC AAG GTT CGG GTT ATC		3318

-Leu Cys Pro Asp Gly Gly Glu Cys Leu Leu Asp Lys Val Arg Val Ile	1080	1085	1090	
CAG GCA GAC ACA TTA AGC CTG ATC CAA GGA GGT ATG ACT GCT GGG AGC				3366
Gln Ala Asp Thr Leu Ser Leu Ile Gln Gly Gly Met Thr Ala Gly Ser				
1095	1100	1105		
ACC ACT TCT GAA ACT AGC TGT GAA ACA GTT CGG CAA TCT TGT GTT GCA				3414
Thr Thr Ser Glu Thr Ser Cys Glu Thr Val Arg Gln Ser Cys Val Ala				
1110	1115	1120		
CTG GTT GAG AAG CTG AAC CCT ATC AAG GAG AGT CTC GAA GCT AAG TCC				3462
Leu Val Glu Lys Leu Asn Pro Ile Lys Glu Ser Leu Glu Ala Lys Ser				
1125	1130	1135		
AAC ACA GTG GAA TGG AGT GCC TTG ATT GCT CAG GCA AGC ATG GCG AGT				3510
Asn Thr Val Glu Trp Ser Ala Leu Ile Ala Gln Ala Ser Met Ala Ser				
1140	1145	1150	1155	
GTG AAC CTA TCA GCA CAG CCG TAC TGG ACT CCT GAT CCA TCT TTC AAG				3558
Val Asn Leu Ser Ala Gln Pro Tyr Trp Thr Pro Asp Pro Ser Phe Lys				
1160	1165	1170		
AGC TAC TTG AAC TAC GGA GCT GGC ACC AGT GAG GTG GAA GTT GAT ATC				3606
Ser Tyr Leu Asn Tyr Gly Ala Gly Thr Ser Glu Val Glu Val Asp Ile				
1175	1180	1185		
CTA ACA GGA GCA ACC ACA ATT CTG CGA AGC GAC CTG GTG TAT GAC TGC				3654
Leu Thr Gly Ala Thr Thr Ile Leu Arg Ser Asp Leu Val Tyr Asp Cys				
1190	1195	1200		
GGG CAG AGC CTA AAC CCT GCT GTA GAC TTG GGC CAG ATC GAG GGC TGC				3702
Gly Gln Ser Leu Asn Pro Ala Val Asp Leu Gly Gln Ile Glu Gly Cys				
1205	1210	1215		
TTT GTC CAA GGA ATA GGG TTC TTC ACG AAC GAG GAC TAC AAG ACG AAT				3750
Phe Val Gln Gly Ile Gly Phe Phe Thr Asn Glu Asp Tyr Lys Thr Asn				
1220	1225	1230	1235	
TCC GAC GGG TTG GTC ATC CAC GAC GGC ACA TGG ACG TAC AAG ATC CCC				3798
Ser Asp Gly Leu Val Ile His Asp Gly Thr Trp Thr Tyr Lys Ile Pro				
1240	1245	1250		
ACG GTG GAT AAT ATC CCG AAG GAG TTC AAT GTT GAG ATG TTT AAC AGC				3846
Thr Val Asp Asn Ile Pro Lys Glu Phe Asn Val Glu Met Phe Asn Ser				
1255	1260	1265		
GCC CCT GAC AAG AAG CGT GTC CTA TCT TCC AAA GCG TCG GGC GAG CCG				3894
Ala Pro Asp Lys Lys Arg Val Leu Ser Ser Lys Ala Ser Gly Glu Pro				
1270	1275	1280		
CCG CTG GTT CTC GCA ACC TCG GTG CAC TGC GCG ATG AGG GAG GCC ATC				3942
Pro Leu Val Leu Ala Thr Ser Val His Cys Ala Met Arg Glu Ala Ile				
1285	1290	1295		
AGG GCG GCG AGG AAG GAG TTC TCG GTC AGC ACC AGC CCC GCG AAA TCC				3990

Arg Ala Ala Arg Lys Glu Phe Ser Val Ser Thr Ser Pro Ala Lys Ser	1300	1305	1310	1315	
GCC GTC ACA TTC CAG ATG GAC GTG CCG GCG ACG ATG CCT GTC GTC AAG					4038
Ala Val Thr Phe Gln Met Asp Val Pro Ala Thr Met Pro Val Val Lys	1320		1325	1330	
GAG CTC TGC GGC CTC GAC GTC GTG GAG AGG TAC CTC GAG AAC GTG TCT					4086
Glu Leu Cys Gly Leu Asp Val Val Glu Arg Tyr Leu Glu Asn Val Ser	1335	1340	1345		
GCC GCC AGT GCC GGC CCA AAC ACA GCG AAA GCA TAGATCCAGC AGGCCTCAGG					4139
Ala Ala Ser Ala Gly Pro Asn Thr Ala Lys Ala	1350	1355			
GTGCAGTCGG CGCACTGCCA GAGATGATGT GTGCTGCCCT GATGTACAGA CAGTACAGTA					4199
CAGAGGAGAG AGAATTGGGG GAACTCAGGA ACTGCGAGGA GCGATGAACA GTATATAGAG					4259
TGAAAAATAA AAGTGCTTCG TACTAATAAT CACTAGAAAA AATTATGCAC ATCTCCCACG					4319
CACTACCGGC ACGACTGTTG AATATTTGT AAAATAAGAT GTCATAAGCT ATTTATTTTC					4379
TGTAAAAAAA AAAAAAAA AAAAAAAA AAA					4412

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1358 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Lys	Glu	Ala	Gly	Ala	Ala	Glu	Ser	Ser	Thr	Val	Val	Leu	Ala
1				5				10						15	
Val	Asn	Gly	Lys	Arg	Tyr	Glu	Ala	Ala	Gly	Val	Ala	Pro	Ser	Thr	Ser
				20				25					30		
Leu	Leu	Glu	Phe	Leu	Arg	Thr	Gln	Thr	Pro	Val	Arg	Gly	Pro	Lys	Leu
				35			40				45				
Gly	Cys	Gly	Glu	Gly	Gly	Cys	Gly	Ala	Cys	Val	Val	Leu	Val	Ser	Lys
				50			55			60					
Tyr	Asp	Pro	Ala	Thr	Asp	Glu	Val	Thr	Glu	Phe	Ser	Ala	Ser	Ser	Cys
				65			70			75					80
Leu	Thr	Leu	Leu	His	Ser	Val	Asp	Arg	Cys	Ser	Val	Thr	Thr	Ser	Glu
				85				90					95		
Gly	Ile	Gly	Asn	Thr	Arg	Asp	Gly	Tyr	His	Pro	Val	Gln	Gln	Arg	Leu

100	105	110
Ser Gly Phe His Ala Ser Gln Cys	Gly Phe Cys Thr Pro Gly Met Cys	
115 120	125	
Met Ser Ile Phe Ser Ala Leu Val Lys Ala Asp Asn Lys Ser Asp Arg		
130 135	140	
Pro Asp Pro Pro Ala Gly Phe Ser Lys Ile Thr Thr Ser Glu Ala Glu		
145 150	155	160
Lys Ala Val Ser Gly Asn Leu Cys Arg Cys Thr Gly Tyr Arg Pro Ile		
165 170	175	
Val Asp Thr Cys Lys Ser Phe Ala Ser Asp Val Asp Leu Glu Asp Leu		
180 185	190	
Gly Leu Asn Cys Phe Trp Lys Lys Gly Glu Glu Pro Ala Glu Val Ser		
195 200	205	
Arg Leu Pro Gly Tyr Asn Ser Gly Ala Val Cys Thr Phe Pro Glu Phe		
210 215	220	
Leu Lys Ser Glu Ile Lys Ser Thr Met Lys Gln Val Asn Asp Val Pro		
225 230	235	240
Ile Ala Ala Ser Gly Asp Gly Trp Tyr His Pro Lys Ser Ile Glu Glu		
245 250	255	
Leu His Arg Leu Phe Asp Ser Ser Trp Phe Asp Asp Ser Ser Val Lys		
260 265	270	
Ile Val Ala Ser Asn Thr Gly Ser Gly Val Tyr Lys Asp Gln Asp Leu		
275 280	285	
Tyr Asp Lys Tyr Ile Asp Ile Lys Gly Ile Pro Glu Leu Ser Val Ile		
290 295	300	
Asn Lys Asn Asp Lys Ala Ile Glu Leu Gly Ser Val Val Ser Ile Ser		
305 310	315	320
Lys Ala Ile Glu Val Leu Ser Asp Gly Asn Leu Val Phe Arg Lys Ile		
325 330	335	
Ala Asp His Leu Asn Lys Val Ala Ser Pro Phe Val Arg Asn Thr Ala		
340 345	350	
Thr Ile Gly Gly Asn Ile Met Met Ala Gln Arg Leu Pro Phe Glu Ser		
355 360	365	
Asp Val Ala Thr Val Leu Leu Ala Ala Gly Ser Thr Val Thr Val Gln		
370 375	380	
Val Ala Ser Lys Arg Leu Cys Phe Thr Leu Glu Glu Phe Leu Glu Gln		
385 390	395	400

-Pro Pro Cys Asp Ser Arg Thr Leu Leu Leu Ser Ile Phe Ile Pro Glu  
 405 410 415  
 Trp Gly Ser Asp Tyr Val Thr Phe Glu Thr Phe Arg Ala Ala Pro Arg  
 420 425 430  
 Pro Phe Gly Asn Ala Val Ser Tyr Val Asn Ser Ala Phe Leu Ala Arg  
 435 440 445  
 Thr Ser Gly Ser Leu Leu Ile Glu Asp Ile Cys Leu Ala Phe Gly Ala  
 450 455 460  
 Tyr Gly Val Asp His Ala Ile Arg Ala Lys Lys Val Glu Asp Phe Leu  
 465 470 475 480  
 Lys Gly Lys Ser Leu Ser Ser Phe Val Ile Leu Glu Ala Ile Lys Leu  
 485 490 495  
 Leu Lys Asp Thr Val Ser Pro Ser Glu Gly Thr Thr His His Glu Tyr  
 500 505 510  
 Arg Val Ser Leu Ala Val Ser Phe Leu Phe Ser Phe Leu Ser Ser Leu  
 515 520 525  
 Ala Asn Ser Ser Ser Ala Pro Ser Asn Ile Asp Thr Pro Asn Gly Ser  
 530 535 540  
 Tyr Thr His Glu Thr Gly Ser Asn Val Asp Ser Pro Glu Arg His Ile  
 545 550 555 560  
 Lys Val Asp Ser Asn Asp Leu Pro Ile Arg Ser Arg Gln Glu Met Val  
 565 570 575  
 Phe Ser Asp Glu Tyr Lys Pro Val Gly Lys Pro Ile Lys Lys Val Gly  
 580 585 590  
 Ala Glu Ile Gln Ala Ser Gly Glu Ala Val Tyr Val Asp Asp Ile Pro  
 595 600 605  
 Ala Pro Lys Asp Cys Leu Tyr Gly Ala Phe Ile Tyr Ser Thr His Pro  
 610 615 620  
 His Ala His Val Arg Ser Ile Asn Phe Lys Ser Ser Leu Ala Ser Gln  
 625 630 635 640  
 Lys Val Ile Thr Val Ile Thr Ala Lys Asp Ile Pro Ser Gly Gly Glu  
 645 650 655  
 Asn Ile Gly Ser Ser Phe Leu Met Gln Gly Glu Ala Leu Phe Ala Asp  
 660 665 670  
 Pro Ile Ala Glu Phe Ala Gly Gln Asn Ile Gly Val Val Ile Ala Glu  
 675 680 685  
 Thr Gln Arg Tyr Ala Asn Met Ala Ala Lys Gln Ala Val Val Glu Tyr  
 690 695 700

Ser Thr Glu Asn Leu Gln Pro Pro Ile Leu Thr Ile Glu Asp Ala Ile  
 705 710 715 720  
 Gln Arg Asn Ser Tyr Ile Gln Ile Pro Pro Phe Leu Ala Pro Lys Pro  
 725 730 735  
 Val Gly Asp Tyr Asn Lys Gly Met Ala Glu Ala Asp His Lys Ile Leu  
 740 745 750  
 Ser Ala Glu Val Lys Leu Glu Ser Gln Tyr Tyr Phe Tyr Met Glu Thr  
 755 760 765  
 Gln Ala Ala Leu Ala Ile Pro Asp Glu Asp Asn Cys Ile Thr Ile Tyr  
 770 775 780  
 Ser Ser Thr Gln Met Pro Glu Leu Thr Gln Asn Leu Ile Ala Arg Cys  
 785 790 795 800  
 Leu Gly Ile Pro Phe His Asn Val Arg Val Ile Ser Arg Arg Val Gly  
 805 810 815  
 Gly Gly Phe Gly Gly Lys Ala Met Lys Ala Thr His Thr Ala Cys Ala  
 820 825 830  
 Cys Ala Leu Ala Ala Phe Lys Leu Arg Arg Pro Val Arg Met Tyr Leu  
 835 840 845  
 Asp Arg Lys Thr Asp Met Ile Met Ala Gly Gly Arg His Pro Met Lys  
 850 855 860  
 Ala Lys Tyr Ser Val Gly Phe Lys Ser Asp Gly Lys Ile Thr Ala Leu  
 865 870 875 880  
 His Leu Asp Leu Gly Ile Asn Ala Gly Ile Ser Pro Asp Val Ser Pro  
 885 890 895  
 Leu Met Pro Arg Ala Ile Ile Gly Ala Leu Lys Lys Tyr Asn Trp Gly  
 900 905 910  
 Thr Leu Glu Phe Asp Thr Lys Val Cys Lys Thr Asn Val Ser Ser Lys  
 915 920 925  
 Ser Ala Met Arg Ala Pro Gly Asp Val Gln Gly Ser Phe Ile Ala Glu  
 930 935 940  
 Ala Ile Ile Glu His Val Ala Ser Ala Leu Ala Leu Asp Thr Asn Thr  
 945 950 955 960  
 Val Arg Arg Lys Asn Leu His Asp Phe Glu Ser Leu Glu Val Phe Tyr  
 965 970 975  
 Gly Glu Ser Ala Gly Glu Ala Ser Thr Tyr Ser Leu Val Ser Met Phe  
 980 985 990  
 Asp Lys Leu Ala Leu Ser Pro Glu Tyr Gln His Arg Ala Ala Met Ile  
 995 1000 1005

-Glu Gln Phe Asn Ser Ser Asn Lys Trp Lys Lys Arg Gly Ile Ser Cys  
 1010 1015 1020  
 Val Pro Ala Thr Tyr Glu Val Asn Leu Arg Pro Thr Pro Gly Lys Val  
 1025 1030 1035 1040  
 Ser Ile Met Asn Asp Gly Ser Ile Ala Val Glu Val Gly Gly Ile Glu  
 1045 1050 1055  
 Ile Gly Gln Gly Leu Trp Thr Lys Val Lys Gln Met Thr Ala Phe Gly  
 1060 1065 1070  
 Leu Gly Gln Leu Cys Pro Asp Gly Gly Glu Cys Leu Leu Asp Lys Val  
 1075 1080 1085  
 Arg Val Ile Gln Ala Asp Thr Leu Ser Leu Ile Gln Gly Gly Met Thr  
 1090 1095 1100  
 Ala Gly Ser Thr Thr Ser Glu Thr Ser Cys Glu Thr Val Arg Gln Ser  
 1105 1110 1115 1120  
 Cys Val Ala Leu Val Glu Lys Leu Asn Pro Ile Lys Glu Ser Leu Glu  
 1125 1130 1135  
 Ala Lys Ser Asn Thr Val Glu Trp Ser Ala Leu Ile Ala Gln Ala Ser  
 1140 1145 1150  
 Met Ala Ser Val Asn Leu Ser Ala Gln Pro Tyr Trp Thr Pro Asp Pro  
 1155 1160 1165  
 Ser Phe Lys Ser Tyr Leu Asn Tyr Gly Ala Gly Thr Ser Glu Val Glu  
 1170 1175 1180  
 Val Asp Ile Leu Thr Gly Ala Thr Thr Ile Leu Arg Ser Asp Leu Val  
 1185 1190 1195 1200  
 Tyr Asp Cys Gly Gln Ser Leu Asn Pro Ala Val Asp Leu Gly Gln Ile  
 1205 1210 1215  
 Glu Gly Cys Phe Val Gln Gly Ile Gly Phe Phe Thr Asn Glu Asp Tyr  
 1220 1225 1230  
 Lys Thr Asn Ser Asp Gly Leu Val Ile His Asp Gly Thr Trp Thr Tyr  
 1235 1240 1245  
 Lys Ile Pro Thr Val Asp Asn Ile Pro Lys Glu Phe Asn Val Glu Met  
 1250 1255 1260  
 Phe Asn Ser Ala Pro Asp Lys Lys Arg Val Leu Ser Ser Lys Ala Ser  
 1265 1270 1275 1280  
 Gly Glu Pro Pro Leu Val Leu Ala Thr Ser Val His Cys Ala Met Arg  
 1285 1290 1295  
 Glu Ala Ile Arg Ala Ala Arg Lys Glu Phe Ser Val Ser Thr Ser Pro  
 1300 1305 1310

- Ala Lys Ser Ala Val Thr Phe Gln Met Asp Val Pro Ala Thr Met Pro  
 1315 1320 1325  
 Val Val Lys Glu Leu Cys Gly Leu Asp Val Val Glu Arg Tyr Leu Glu  
 1330 1335 1340  
 Asn Val Ser Ala Ala Ser Ala Gly Pro | Asn Thr Ala Lys Ala  
 1345 1350 1355

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: maize (Zea mays L.)
- (B) STRAIN: cultivar: Golden Cross Bantam 70

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 91..4137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGGCTCTCT CGGTGCAGAC GTCCGGGACT AGTACGTGGA TCGGGCCGGG GGCAACTCGA	60
GTCTCAAGA AGGCTGCTAC CTGCTAGAGG ATG GAG ATG GGG AAG GCG GCG GCG	114
Met Glu Met Gly Lys Ala Ala Ala	
1360 1365	
GTG GTG CTG GCG GTG AAC GGC AAG CGG TAC GAG GCC GCC GGC GTG GAC	162
Val Val Leu Ala Val Asn Gly Lys Arg Tyr Glu Ala Ala Gly Val Asp	
1370 1375 1380	
CCG TCG ACG ACG CTG CTG GAG TTC CTG CGC ACC CAC ACG CCC GTC AGG	210
Pro Ser Thr Thr Leu Leu Glu Phe Leu Arg Thr His Thr Pro Val Arg	
1385 1390 1395	
GGG CCC AAG CTC GGC TGC GGC GAA GGT GGC TGC GGT GCA TGC GTT GTG	258
Gly Pro Lys Leu Gly Cys Gly Glu Gly Cys Gly Ala Cys Val Val	
1400 1405 1410	
CTT GTC TCG AAG TAC GAC CCA GCC ACC GAC GAG GTG ACC GAG TTC TCA	306
Leu Val Ser Lys Tyr Asp Pro Ala Thr Asp Glu Val Thr Glu Phe Ser	
1415 1420 1425 1430	
GCG AGC TCC TGC CTG ACG CTG CTC CAT AGC GTG GAC CGC TGC TCG GTG	354
Ala Ser Ser Cys Leu Thr Leu Leu His Ser Val Asp Arg Cys Ser Val	

1435	1440	1445	
ACC ACC AGC GAG GGC ATT GGC AAC ACC AAG GAT GGC TAC CAC CCT GTG Thr Thr Ser Glu Gly Ile Gly Asn Thr Lys Asp Gly Tyr His Pro Val 1450	1455	1460	402
CAG CAG CGC CTC TCC GGC TTC CAC GCC TCC CAG TGC GGT TTC TGC ACG Gln Gln Arg Leu Ser Gly Phe His Ala Ser Gln Cys Gly Phe Cys Thr 1465	1470	1475	450
CCC GGC ATG TGC ATG TCC ATC TTC TCT GCG CTT GTC AAA GCC GAC AAG Pro Gly Met Cys Met Ser Ile Phe Ser Ala Leu Val Lys Ala Asp Lys 1480	1485	1490	498
GCG GCC AAC CGG CCA GCC CCA CCG GCC GGC TTC TCC AAG CTC ACT TCC Ala Ala Asn Arg Pro Ala Pro Pro Ala Gly Phe Ser Lys Leu Thr Ser 1495	1500	1505	546
TCG GAG GCT GAG AAG GCT GTC TCT GGC AAC CTG TGC CGC TGC ACA GGG Ser Glu Ala Glu Lys Ala Val Ser Gly Asn Leu Cys Arg Cys Thr Gly 1515	1520	1525	594
TAC AGG CCC ATC GTC GAC GCC TGT AAG AGC TTC GCA GCC GAT GTT GAT Tyr Arg Pro Ile Val Asp Ala Cys Lys Ser Phe Ala Ala Asp Val Asp 1530	1535	1540	642
CTT GAG GAC CTG GGC CTC AAC TGC TTC TGG AAG AAG GGT GAT GAG CCT Leu Glu Asp Leu Gly Leu Asn Cys Phe Trp Lys Lys Gly Asp Glu Pro 1545	1550	1555	690
GCA GAT GTC AGC AAG CTG CCA GGC TAC AAC AGT GGT GAC GTC TGC ACT Ala Asp Val Ser Lys Leu Pro Gly Tyr Asn Ser Gly Asp Val Cys Thr 1560	1565	1570	738
TTC CCT GAC TTT CTC AAA TCT GAG ATG AAG TCC TCA ATT CAG CAG GCT Phe Pro Asp Phe Leu Lys Ser Glu Met Lys Ser Ser Ile Gln Gln Ala 1575	1580	1585	786
AAC AGC GCT CCA GTT CCT GTT TCT GAC GAC GGC TGG TAC CGT CCT AGG Asn Ser Ala Pro Val Pro Val Ser Asp Asp Gly Trp Tyr Arg Pro Arg 1595	1600	1605	834
AGC ATT GAC GAG CTT CAC AGG TTG TTT CAA TCT AGC TCC TTC GAT GAA Ser Ile Asp Glu Leu His Arg Leu Phe Gln Ser Ser Phe Asp Glu 1610	1615	1620	882
AAT TCC GTG AAG ATA GTG GCT TCA AAC ACT GGG TCT GGA GTG TAC AAG Asn Ser Val Lys Ile Val Ala Ser Asn Thr Gly Ser Gly Val Tyr Lys 1625	1630	1635	930
GAT CAG GAC CTT TAT GAC AAG TAC ATT GAC ATC AAA GGA ATC CCA GAG Asp Gln Asp Leu Tyr Asp Lys Tyr Ile Asp Ile Lys Gly Ile Pro Glu 1640	1645	1650	978
CTT TCA GTC ATC AAC AGA AAC GAC AAA GGA ATT GAG CTT GGA TCA GTT Leu Ser Val Ile Asn Arg Asn Asp Lys Gly Ile Glu Leu Gly Ser Val			1026

1655	1660	1665	1670	
GTG TCC ATC TCT AAA GCT ATT GAG GTG CTG TCA GAT GGA AAT CTC GTC Val Ser Ile Ser Lys Ala Ile Glu Val Leu Ser Asp Gly Asn Leu Val 1675		1680	1685	1074
TTC AGA AAG ATT GCT GGT CAC CTG AAC AAA GTG GCT TCA CCG TTT GTT Phe Arg Lys Ile Ala Gly His Leu Asn Lys Val Ala Ser Pro Phe Val 1690	1695		1700	1122
CGG AAC ACT GCA ACC ATA GGT GGA AAC ATA GTC ATG GCA CAA AGA TTG Arg Asn Thr Ala Thr Ile Gly Gly Asn Ile Val Met Ala Gln Arg Leu 1705	1710		1715	1170
CCA TTC GCA TCG GAC ATT GCA ACC ATA CTA CTA GCT GCA GGT TCA ACA Pro Phe Ala Ser Asp Ile Ala Thr Ile Leu Leu Ala Ala Gly Ser Thr 1720	1725		1730	1218
GTC ACA ATC CAG GTG GCT TCC AAA AGG CTG TGC TTC ACT CTG GAG GAG Val Thr Ile Gln Val Ala Ser Lys Arg Leu Cys Phe Thr Leu Glu Glu 1735	1740	1745	1750	1266
TTC TTG CAG CAG CCT CCA TGC GAT TCT AGG ACC CTG CTG CTG AGC ATA Phe Leu Gln Gln Pro Pro Cys Asp Ser Arg Thr Leu Leu Leu Ser Ile 1755		1760	1765	1314
TTT ATC CCG GAA TGG GGC TCA AAT GAT GTC ACC TTT GAG ACT TTC CGA Phe Ile Pro Glu Trp Gly Ser Asn Asp Val Thr Phe Glu Thr Phe Arg 1770	1775		1780	1362
GCA GCA CCT CGT CCA CTT GGC AAT GCT GTC TCA TAT GTC AAT TCA GCT Ala Ala Pro Arg Pro Leu Gly Asn Ala Val Ser Tyr Val Asn Ser Ala 1785	1790		1795	1410
TTC TTG GCA AGG ACT TCA TTG GAT GCA GCA TCA AAG GAC CAT CTC ATC Phe Leu Ala Arg Thr Ser Leu Asp Ala Ala Ser Lys Asp His Leu Ile 1800	1805		1810	1458
GAG GAT ATA TGT CTG GCG TTC GGT GCT TAT GGA GCT GAT CAT GCT ATT Glu Asp Ile Cys Leu Ala Phe Gly Ala Tyr Gly Ala Asp His Ala Ile 1815	1820	1825	1830	1506
AGA GCT AGA AAG GTT GAG GAT TAC CTG AAG GGC AAA ACA GTG AGC TCG Arg Ala Arg Lys Val Glu Asp Tyr Leu Lys Gly Lys Thr Val Ser Ser 1835	1840		1845	1554
TCT GTC ATA CTT GAA GCT GTT CGG TTG CTT AAA GGG TCT ATT AAA CCA Ser Val Ile Leu Glu Ala Val Arg Leu Leu Lys Gly Ser Ile Lys Pro 1850	1855		1860	1602
TCA GAA GGC TCA ACA CAT CCT GAG TAT AGA ATT AGC TTG GCT GTC AGT Ser Glu Gly Ser Thr His Pro Glu Tyr Arg Ile Ser Leu Ala Val Ser 1865	1870		1875	1650
TTC TTG TTT ACC TTC CTA TCC CTT GCC AAC AGC TTG AAT GAA TCT Phe Leu Phe Thr Phe Leu Ser Ser Leu Ala Asn Ser Leu Asn Glu Ser				1698

1880	1885	1890	
GCA AAG GTT AGT GGT ACC AAC GAG CAC TCA CCA GAG AAG CAA CTC AAG Ala Lys Val Ser Gly Thr Asn Glu His Ser Pro Glu Lys Gln Leu Lys 1895 1900 1905 1910			1746
TTG GAC ATC AAT GAT TTG CCA ATA CGA TCA AGA CAA GAA ATA TTT TTC Leu Asp Ile Asn Asp Leu Pro Ile Arg Ser Arg Gln Glu Ile Phe Phe 1915 1920 1925			1794
ACT GAT GCA TAT AAG CCA GTT GGC AAA GCA ATT AAG AAA GCT GGG GTA Thr Asp Ala Tyr Lys Pro Val Gly Lys Ala Ile Lys Lys Ala Gly Val 1930 1935 1940			1842
GAG ATC CAA GCT TCA GGG GAA GCT GTG TAC GTT GAT GAT ATC CCT GCT Glu Ile Gln Ala Ser Gly Glu Ala Val Tyr Val Asp Asp Ile Pro Ala 1945 1950 1955			1890
CCC AAA GAT TGC CTC TAT GGG GCA TTT ATT TAT AGC ACA CAC CCT CAT Pro Lys Asp Cys Leu Tyr Gly Ala Phe Ile Tyr Ser Thr His Pro His 1960 1965 1970			1938
GCA CAT GTA AAG TCA ATC AAC TTT AAA CCA TCT TTG GCT TCA CAG AAG Ala His Val Lys Ser Ile Asn Phe Lys Pro Ser Leu Ala Ser Gln Lys 1975 1980 1985 1990			1986
ATC ATC ACA GTT ATC ACT GCA AAG GAT ATT CCC AGC GGT GGA CAA AAT Ile Ile Thr Val Ile Thr Ala Lys Asp Ile Pro Ser Gly Gly Gln Asn 1995 2000 2005			2034
GTT GGT TAT AGC TTC CCG ATG ATT GGA GAA GAA GCA CTT TTT GCA GAT Val Gly Tyr Ser Phe Pro Met Ile Gly Glu Glu Ala Leu Phe Ala Asp 2010 2015 2020			2082
CCA GTT GCT GAA TTT GCT GGT CAA AAT ATT GGT GTC GTG ATT GCT CAA Pro Val Ala Glu Phe Ala Gly Gln Asn Ile Gly Val Val Ile Ala Gln 2025 2030 2035			2130
ACA CAG AAG TAT GCC TAC ATG GCG GCA AAG CAA GCC ATC ATT GAG TAT Thr Gln Lys Tyr Ala Tyr Met Ala Ala Lys Gln Ala Ile Ile Glu Tyr 2040 2045 2050			2178
AGC ACA GAA AAT CTG CAG CCA CCA ATT CTG ACA ATA GAA GAT GCA ATT Ser Thr Glu Asn Leu Gln Pro Pro Ile Leu Thr Ile Glu Asp Ala Ile 2055 2060 2065 2070			2226
GAA CGA AGC AGC TTC TTC CAA ACC CTC CCA TTT GTA GCT CCT AAG CCA Glu Arg Ser Ser Phe Phe Gln Thr Leu Pro Phe Val Ala Pro Lys Pro 2075 2080 2085			2274
GTT GGT GAT TAC GAC AAA GGG ATG TCT GAA GCT GAT CAC AAG ATT TTA Val Gly Asp Tyr Asp Lys Gly Met Ser Glu Ala Asp His Lys Ile Leu 2090 2095 2100			2322
TCG GCA GAG GTA AAA ATT GAA TCC CAA TAC TTT TTC TAC ATG GAG CCA Ser Ala Glu Val Lys Ile Glu Ser Gln Tyr Phe Phe Tyr Met Glu Pro			2370

2105	2110	2115	
CAA GTG GCG CTA GCT ATT CCT GAT GAA GAT AAC TGC ATA ACC ATC TAT Gln Val Ala Leu Ala Ile Pro Asp Glu Asp Asn Cys Ile Thr Ile Tyr 2120	2125	2130	2418
TTT TCG ACA CAA TTA CCT GAG TCC ACA CAA AAT GTG GTT GCA AAG TGC Phe Ser Thr Gln Leu Pro Glu Ser Thr Gln Asn Val Val Ala Lys Cys 2135	2140	2145	2466
GTT GGC ATT CCA TTT CAC AAT GTC CGT GTA ATC ACC AGA AGG GTC GGA Val Gly Ile Pro Phe His Asn Val Arg Val Ile Thr Arg Arg Val Gly 2155	2160	2165	2514
GGA GGC TTT GGT GGA AAA GCA TTG AAA TCA ATG CAT GTT GCA TGT GCA Gly Gly Phe Gly Gly Lys Ala Leu Lys Ser Met His Val Ala Cys Ala 2170	2175	2180	2562
TGT GCA GTT GCT GCA TTG AAG CTA CAA CGT CCA GTT CGG ATG TAC CTC Cys Ala Val Ala Ala Leu Lys Leu Gln Arg Pro Val Arg Met Tyr Leu 2185	2190	2195	2610
GAT CGC AAG ACA GAC ATG ATA ATG GCA GGC GGG CGG CAT CCT ATG AAG Asp Arg Lys Thr Asp Met Ile Met Ala Gly Gly Arg His Pro Met Lys 2200	2205	2210	2658
GTG AAG TAC TCT GTT GGG TTC AAG TCA AAC GGC AAG ATC ACA GCC TTA Val Lys Tyr Ser Val Gly Phe Lys Ser Asn Gly Lys Ile Thr Ala Leu 2215	2220	2225	2706
CAT CTT GAT CTT GGG ATC AAT GGT GGA ATA TCT CCA GAT ATG AGT CCA His Leu Asp Leu Gly Ile Asn Gly Gly Ile Ser Pro Asp Met Ser Pro 2235	2240	2245	2754
ATG ATT GCA GCA CCT GTC ATA GGT TCT CTC AAA AAG TAC AAC TGG GGC Met Ile Ala Ala Pro Val Ile Gly Ser Leu Lys Lys Tyr Asn Trp Gly 2250	2255	2260	2802
AAT CTT GCA TTT GAC ACC AAG GTC TGC AAA ACA AAT GTC TCA TCA AAA Asn Leu Ala Phe Asp Thr Lys Val Cys Lys Thr Asn Val Ser Ser Lys 2265	2270	2275	2850
TCG TCA ATG AGA GCT CCT GGA GAT GCG CAG GGC TCT TTC ATT GCT GAA Ser Ser Met Arg Ala Pro Gly Asp Ala Gln Gly Ser Phe Ile Ala Glu 2280	2285	2290	2898
GCC ATC ATC GAG CAT GTT GCC TCG GCA CTT TCA GCC GAC ACT AAT ACC Ala Ile Ile Glu His Val Ala Ser Ala Leu Ser Ala Asp Thr Asn Thr 2295	2300	2305	2946
ATA AGG AGA AAG AAC CTT CAT GAC TTT GAG AGC CTT GCA GTG TTC TTT Ile Arg Arg Lys Asn Leu His Asp Phe Glu Ser Leu Ala Val Phe Phe 2315	2320	2325	2994
GGA GAT AGT GCA GGT GAA GCT TCT ACA TAC AGC CTT GTC ACC ATG TTC Gly Asp Ser Ala Gly Glu Ala Ser Thr Tyr Ser Leu Val Thr Met Phe			3042

2330	2335	2340	
GAT AAA TTG GCC TCC TCT CCA GAA TAC CAG CAC CGA GCT GAA ATG GTG Asp Lys Leu Ala Ser Ser Pro Glu Tyr Gln His Arg Ala Glu Met Val 2345	2350	2355	3090
GAA CAA TTC AAC CGA AGC AAC AAG TGG AAG AAG CGT GGC ATT TCT TGT Glu Gln Phe Asn Arg Ser Asn Lys Trp Lys Lys Arg Gly Ile Ser Cys 2360	2365	2370	3138
GTG CCT GTA ACA TAT GAG GTG CAG CTT CGG CCA ACT CCA GGA AAG GTG Val Pro Val Thr Tyr Glu Val Gln Leu Arg Pro Thr Pro Gly Lys Val 2375	2380	2385	3186
TCT ATC ATG AAT GAT GGT TCC ATT GCT GTT GAG GTT GGA GGG GTT GAG Ser Ile Met Asn Asp Gly Ser Ile Ala Val Glu Val Gly Gly Val Glu 2395	2400	2405	3234
CTA GGC CAA GGG TTG TGG ACA AAA GTG AAG CAG ATG ACG GCA TTC GGA Leu Gly Gln Gly Leu Trp Thr Lys Val Lys Gln Met Thr Ala Phe Gly 2410	2415	2420	3282
CTA GGA CAG CTG TGT CCT GGC GGC GGT GAA AGC CTT CTA GAC AAG GTG Leu Gly Gln Leu Cys Pro Gly Gly Glu Ser Leu Leu Asp Lys Val 2425	2430	2435	3330
CGG GTC ATC CAG GCC GAC ACA TTG AGC ATG ATC CAA GGA GGG GTC ACT Arg Val Ile Gln Ala Asp Thr Leu Ser Met Ile Gln Gly Gly Val Thr 2440	2445	2450	3378
GGT GGG AGC ACC ACT TCT GAA ACT AGC TGT GAA GCA GTT CGT AAG TCG Gly Gly Ser Thr Thr Ser Glu Thr Ser Cys Glu Ala Val Arg Lys Ser 2455	2460	2465	3426
TGT GTT GCA CTC GTC GAG AGC TTG AAG CCA ATC AAG GAG AAT CTG GAG Cys Val Ala Leu Val Glu Ser Leu Lys Pro Ile Lys Glu Asn Leu Glu 2475	2480	2485	3474
GCT AAA ACT GGC ACA GTG GAA TGG AGT GCC TTG ATT GCA CAG GCA AGT Ala Lys Thr Gly Thr Val Glu Trp Ser Ala Leu Ile Ala Gln Ala Ser 2490	2495	2500	3522
ATG GCG AGC GTT AAC TTA TCG GCA CAT GCA TAC TGG ACC CCT GAT CCA Met Ala Ser Val Asn Leu Ser Ala His Ala Tyr Trp Thr Pro Asp Pro 2505	2510	2515	3570
ACT TTC ACA AGC TAT TTG AAC TAC GGA GCC GGC ACT AGC GAG GTG GAA Thr Phe Thr Ser Tyr Leu Asn Tyr Gly Ala Gly Thr Ser Glu Val Glu 2520	2525	2530	3618
ATT GAT GTC CTG ACA GGA GCA ACA ACA ATT CTA AGG AGT GAC CTT GTC Ile Asp Val Leu Thr Gly Ala Thr Thr Ile Leu Arg Ser Asp Leu Val 2535	2540	2545	3666
TAC GAT TGC GGG CAA AGC TTG AAC CCT GCT GTC GAT TTG GGG CAG GTG Tyr Asp Cys Gly Gln Ser Leu Asn Pro Ala Val Asp Leu Gly Gln Val			3714

2555	2560	2565	
GAA GGT GCA TTC GTA CAA GGA GTA GGC TTC TTC ACA AAC GAG GAG TAC Glu Gly Ala Phe Val Gln Gly Val Gly Phe Phe Thr Asn Glu Glu Tyr 2570	2575	2580	3762
GCA ACC AAC TCT GAC GGG TTG GTC ATC CAC GAT GGC ACA TGG ACG TAC Ala Thr Asn Ser Asp Gly Leu Val Ile His Asp Gly Thr Trp Thr Tyr 2585	2590	2595	3810
AAG ATC CCC ACG GTC GAC ACC ATC CCA AAG CAG TTC AAC GTT GAG CTG Lys Ile Pro Thr Val Asp Thr Ile Pro Lys Gln Phe Asn Val Glu Leu 2600	2605	2610	3858
ATC AAC AGC GCC CGT GAC CAG AAG CGC GTC CTC TCT TCC AAA GCA TCG Ile Asn Ser Ala Arg Asp Gln Lys Arg Val Leu Ser Ser Lys Ala Ser 2615	2620	2625	3906
GGC GAG CCT CCG CTT CTC CTA GCT TCC TCT GTG CAC TGC GCA ATG AGG Gly Glu Pro Pro Leu Leu Leu Ala Ser Ser Val His Cys Ala Met Arg 2635	2640	2645	3954
GAG GCC ATC AGG GCC AGG AAA GAA TTC TCG GTC TGC ACT GGT CCA Glu Ala Ile Arg Ala Ala Arg Lys Glu Phe Ser Val Cys Thr Gly Pro 2650	2655	2660	4002
GCG AAC TCC GCC ATC ACG TTC CAG ATG GAC GTG CCG GCA ACG ATG CCT Ala Asn Ser Ala Ile Thr Phe Gln Met Asp Val Pro Ala Thr Met Pro 2665	2670	2675	4050
GTC GTC AAG GAG CTC TGC GGC CTG GAT GTC GTT GAG AGG TAC CTG GAG Val Val Lys Glu Leu Cys Gly Leu Asp Val Val Glu Arg Tyr Leu Glu 2680	2685	2690	4098
AGC GTG TCG GCT GCC AGC CCA ACA AAC ACC GCT AAA GCA TAGATCCAGT Ser Val Ser Ala Ala Ser Pro Thr Asn Thr Ala Lys Ala 2695	2700	2705	4147
AGGCGCTCTA TCCATGGTGT GATGGCTTAA TCAATCTGTA AAACACTAAG CGGCGTGACA			4207
TGCCGAGCTT TCAGTGTAG CTATGATGTA CAGAAGAAGA GGTACCAATG GCGAGTTGTG			4267
GCCATGCGAA TCAGGAGTCA TGAACCATTG AGGGGGAAA TAAAGTAAAT AAGTGTGCG			4327
CCGGCGAAAA AAAAAAAA AAAAAAAA AA			4359

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1349 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Met Gly Lys Ala Ala Ala Val Val Leu Ala Val Asn Gly Lys  
1 5 10 15

Arg Tyr Glu Ala Ala Gly Val Asp Pro Ser Thr Thr Leu Leu Glu Phe  
20 25 30

Leu Arg Thr His Thr Pro Val Arg Gly Pro Lys Leu Gly Cys Gly Glu  
35 40 45

Gly Gly Cys Gly Ala Cys Val Val Leu Val Ser Lys Tyr Asp Pro Ala  
50 55 60

Thr Asp Glu Val Thr Glu Phe Ser Ala Ser Ser Cys Leu Thr Leu Leu  
65 70 75 80

His Ser Val Asp Arg Cys Ser Val Thr Thr Ser Glu Gly Ile Gly Asn  
85 90 95

Thr Lys Asp Gly Tyr His Pro Val Gln Gln Arg Leu Ser Gly Phe His  
100 105 110

Ala Ser Gln Cys Gly Phe Cys Thr Pro Gly Met Cys Met Ser Ile Phe  
115 120 125

Ser Ala Leu Val Lys Ala Asp Lys Ala Ala Asn Arg Pro Ala Pro Pro  
130 135 140

Ala Gly Phe Ser Lys Leu Thr Ser Ser Glu Ala Glu Lys Ala Val Ser  
145 150 155 160

Gly Asn Leu Cys Arg Cys Thr Gly Tyr Arg Pro Ile Val Asp Ala Cys  
165 170 175

Lys Ser Phe Ala Ala Asp Val Asp Leu Glu Asp Leu Gly Leu Asn Cys  
180 185 190

Phe Trp Lys Lys Gly Asp Glu Pro Ala Asp Val Ser Lys Leu Pro Gly  
195 200 205

Tyr Asn Ser Gly Asp Val Cys Thr Phe Pro Asp Phe Leu Lys Ser Glu  
210 215 220

Met Lys Ser Ser Ile Gln Gln Ala Asn Ser Ala Pro Val Pro Val Ser  
225 230 235 240

Asp Asp Gly Trp Tyr Arg Pro Arg Ser Ile Asp Glu Leu His Arg Leu  
245 250 255

Phe Gln Ser Ser Ser Phe Asp Glu Asn Ser Val Lys Ile Val Ala Ser  
260 265 270

Asn Thr Gly Ser Gly Val Tyr Lys Asp Gln Asp Leu Tyr Asp Lys Tyr  
275 280 285

- Ile Asp Ile Lys Gly Ile Pro Glu Leu Ser Val Ile Asn Arg Asn Asp  
 290 295 300  
 Lys Gly Ile Glu Leu Gly Ser Val Val Ser Ile Ser Lys Ala Ile Glu  
 305 310 315 320  
 Val Leu Ser Asp Gly Asn Leu Val Phe Arg Lys Ile Ala Gly His Leu  
 325 330 335  
 Asn Lys Val Ala Ser Pro Phe Val Arg Asn Thr Ala Thr Ile Gly Gly  
 340 345 350  
 Asn Ile Val Met Ala Gln Arg Leu Pro Phe Ala Ser Asp Ile Ala Thr  
 355 360 365  
 Ile Leu Leu Ala Ala Gly Ser Thr Val Thr Ile Gln Val Ala Ser Lys  
 370 375 380  
 Arg Leu Cys Phe Thr Leu Glu Glu Phe Leu Gln Gln Pro Pro Cys Asp  
 385 390 395 400  
 Ser Arg Thr Leu Leu Leu Ser Ile Phe Ile Pro Glu Trp Gly Ser Asn  
 405 410 415  
 Asp Val Thr Phe Glu Thr Phe Arg Ala Ala Pro Arg Pro Leu Gly Asn  
 420 425 430  
 Ala Val Ser Tyr Val Asn Ser Ala Phe Leu Ala Arg Thr Ser Leu Asp  
 435 440 445  
 Ala Ala Ser Lys Asp His Leu Ile Glu Asp Ile Cys Leu Ala Phe Gly  
 450 455 460  
 Ala Tyr Gly Ala Asp His Ala Ile Arg Ala Arg Lys Val Glu Asp Tyr  
 465 470 475 480  
 Leu Lys Gly Lys Thr Val Ser Ser Val Ile Leu Glu Ala Val Arg  
 485 490 495  
 Leu Leu Lys Gly Ser Ile Lys Pro Ser Glu Gly Ser Thr His Pro Glu  
 500 505 510  
 Tyr Arg Ile Ser Leu Ala Val Ser Phe Leu Phe Thr Phe Leu Ser Ser  
 515 520 525  
 Leu Ala Asn Ser Leu Asn Glu Ser Ala Lys Val Ser Gly Thr Asn Glu  
 530 535 540  
 His Ser Pro Glu Lys Gln Leu Lys Leu Asp Ile Asn Asp Leu Pro Ile  
 545 550 555 560  
 Arg Ser Arg Gln Glu Ile Phe Phe Thr Asp Ala Tyr Lys Pro Val Gly  
 565 570 575  
 Lys Ala Ile Lys Lys Ala Gly Val Glu Ile Gln Ala Ser Gly Glu Ala  
 580 585 590

- Val Tyr Val Asp Asp Ile Pro Ala Pro Lys Asp Cys Leu Tyr Gly Ala  
 595 600 605  
 Phe Ile Tyr Ser Thr His Pro His Ala His Val Lys Ser Ile Asn Phe  
 610 615 620  
 Lys Pro Ser Leu Ala Ser Gln Lys Ile Ile Thr Val Ile Thr Ala Lys  
 625 630 635 640  
 Asp Ile Pro Ser Gly Gly Gln Asn Val Gly Tyr Ser Phe Pro Met Ile  
 645 650 655  
 Gly Glu Glu Ala Leu Phe Ala Asp Pro Val Ala Glu Phe Ala Gly Gln  
 660 665 670  
 Asn Ile Gly Val Val Ile Ala Gln Thr Gln Lys Tyr Ala Tyr Met Ala  
 675 680 685  
 Ala Lys Gln Ala Ile Ile Glu Tyr Ser Thr Glu Asn Leu Gln Pro Pro  
 690 695 700  
 Ile Leu Thr Ile Glu Asp Ala Ile Glu Arg Ser Ser Phe Phe Gln Thr  
 705 710 715 720  
 Leu Pro Phe Val Ala Pro Lys Pro Val Gly Asp Tyr Asp Lys Gly Met  
 725 730 735  
 Ser Glu Ala Asp His Lys Ile Leu Ser Ala Glu Val Lys Ile Glu Ser  
 740 745 750  
 Gln Tyr Phe Phe Tyr Met Glu Pro Gln Val Ala Leu Ala Ile Pro Asp  
 755 760 765  
 Glu Asp Asn Cys Ile Thr Ile Tyr Phe Ser Thr Gln Leu Pro Glu Ser  
 770 775 780  
 Thr Gln Asn Val Val Ala Lys Cys Val Gly Ile Pro Phe His Asn Val  
 785 790 795 800  
 Arg Val Ile Thr Arg Arg Val Gly Gly Phe Gly Gly Lys Ala Leu  
 805 810 815  
 Lys Ser Met His Val Ala Cys Ala Cys Ala Val Ala Ala Leu Lys Leu  
 820 825 830  
 Gln Arg Pro Val Arg Met Tyr Leu Asp Arg Lys Thr Asp Met Ile Met  
 835 840 845  
 Ala Gly Gly Arg His Pro Met Lys Val Lys Tyr Ser Val Gly Phe Lys  
 850 855 860  
 Ser Asn Gly Lys Ile Thr Ala Leu His Leu Asp Leu Gly Ile Asn Gly  
 865 870 875 880  
 Gly Ile Ser Pro Asp Met Ser Pro Met Ile Ala Ala Pro Val Ile Gly  
 885 890 895

-Ser Leu Lys Lys Tyr Asn Trp Gly Asn Leu Ala Phe Asp Thr Lys Val  
 900 905 910  
 Cys Lys Thr Asn Val Ser Ser Lys Ser Ser Met Arg Ala Pro Gly Asp  
 915 920 925  
 Ala Gln Gly Ser Phe Ile Ala Glu Ala Ile Ile Glu His Val Ala Ser  
 930 935 940  
 Ala Leu Ser Ala Asp Thr Asn Thr Ile Arg Arg Lys Asn Leu His Asp  
 945 950 955 960  
 Phe Glu Ser Leu Ala Val Phe Phe Gly Asp Ser Ala Gly Glu Ala Ser  
 965 970 975  
 Thr Tyr Ser Leu Val Thr Met Phe Asp Lys Leu Ala Ser Ser Pro Glu  
 980 985 990  
 Tyr Gln His Arg Ala Glu Met Val Glu Gln Phe Asn Arg Ser Asn Lys  
 995 1000 1005  
 Trp Lys Lys Arg Gly Ile Ser Cys Val Pro Val Thr Tyr Glu Val Gln  
 1010 1015 1020  
 Leu Arg Pro Thr Pro Gly Lys Val Ser Ile Met Asn Asp Gly Ser Ile  
 1025 1030 1035 1040  
 Ala Val Glu Val Gly Gly Val Glu Leu Gly Gln Gly Leu Trp Thr Lys  
 1045 1050 1055  
 Val Lys Gln Met Thr Ala Phe Gly Leu Gly Gln Leu Cys Pro Gly Gly  
 1060 1065 1070  
 Gly Glu Ser Leu Leu Asp Lys Val Arg Val Ile Gln Ala Asp Thr Leu  
 1075 1080 1085  
 Ser Met Ile Gln Gly Gly Val Thr Gly Gly Ser Thr Thr Ser Glu Thr  
 1090 1095 1100  
 Ser Cys Glu Ala Val Arg Lys Ser Cys Val Ala Leu Val Glu Ser Leu  
 1105 1110 1115 1120  
 Lys Pro Ile Lys Glu Asn Leu Glu Ala Lys Thr Gly Thr Val Glu Trp  
 1125 1130 1135  
 Ser Ala Leu Ile Ala Gln Ala Ser Met Ala Ser Val Asn Leu Ser Ala  
 1140 1145 1150  
 His Ala Tyr Trp Thr Pro Asp Pro Thr Phe Thr Ser Tyr Leu Asn Tyr  
 1155 1160 1165  
 Gly Ala Gly Thr Ser Glu Val Glu Ile Asp Val Leu Thr Gly Ala Thr  
 1170 1175 1180  
 Thr Ile Leu Arg Ser Asp Leu Val Tyr Asp Cys Gly Gln Ser Leu Asn  
 1185 1190 1195 1200

Pro Ala Val Asp Leu Gly Gln Val Glu Gly Ala Phe Val Gln Gly Val  
 1205 1210 1215  
 Gly Phe Phe Thr Asn Glu Glu Tyr Ala Thr Asn Ser Asp Gly Leu Val  
 1220 1225 1230  
 Ile His Asp Gly Thr Trp Thr Tyr Lys Ile Pro Thr Val Asp Thr Ile  
 1235 1240 1245  
 Pro Lys Gln Phe Asn Val Glu Leu Ile Asn Ser Ala Arg Asp Gln Lys  
 1250 1255 1260  
 Arg Val Leu Ser Ser Lys Ala Ser Gly Glu Pro Pro Leu Leu Leu Ala  
 1265 1270 1275 1280  
 Ser Ser Val His Cys Ala Met Arg Glu Ala Ile Arg Ala Ala Arg Lys  
 1285 1290 1295  
 Glu Phe Ser Val Cys Thr Gly Pro Ala Asn Ser Ala Ile Thr Phe Gln  
 1300 1305 1310  
 Met Asp Val Pro Ala Thr Met Pro Val Val Lys Glu Leu Cys Gly Leu  
 1315 1320 1325  
 Asp Val Val Glu Arg Tyr Leu Glu Ser Val Ser Ala Ala Ser Pro Thr  
 1330 1335 1340  
 Asn Thr Ala Lys Ala  
 1345

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide primer (23-mer in anti-sense orientation)"
- (ix) FEATURE:
  - (A) NAME/KEY: modified\_base
  - (B) LOCATION: 6
  - (D) OTHER INFORMATION: /mod\_base= i
- (ix) FEATURE:
  - (A) NAME/KEY: modified\_base
  - (B) LOCATION: 9
  - (D) OTHER INFORMATION: /mod\_base= i
- (ix) FEATURE:
  - (A) NAME/KEY: modified\_base
  - (B) LOCATION: 18

(D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCANGTNC CRTCTTGNAT NAC

23

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide primer  
(23-mer in sense orientation)"

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGNGARGCNG TNTAYGTNGA YGA

23

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide primer  
(sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTGGTCAAA ATATTGGTGT CGTGATTG

28

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide primer  
(sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATTGCTGAA ACACAAAGAT ATGCTAAT

28

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide primer  
(anti-sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGGCTGCAGA TTTTCTGTGC TATACTC

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide primer  
(anti-sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGCTTGCAG CCATATTAGC ATATCTT

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide primer  
(anti-sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACAGCCTTT GGAAGCCACC TGGA

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide primer  
(anti-sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATCGGACTTG TTGTCGGCCT TGAC

24

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide primer  
(sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATTGCTCAA ACACAGAAAGT ATGCCTAC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide primer  
(anti-sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTTGCCGCC ATGTAGGCAT ACTTC

25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide primer  
(anti-sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTCCACCTAT GGTTGCAGTG TTCC

24